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5. (Twice amended) The pullulanase of Claim 6, wherein the *B. deramificans* pullulanase has the designation T89.117D in the LMG culture collection.

6. (Twice amended) A truncated *Bacillus* pullulanase comprising a deletion of about 100 amino acids from the amino terminus of a *Bacillus* pullulanase wherein the *Bacillus* is selected from the group consisting of *B. subtilis*, *B. deramificans*, *B. stearothermophilus*, *B. naganoensis*, *B. flavocaldarius*, *B. acidopullulyticus*, *Bacillus* sp APC-9603, *B. sectorramus*, *B. cereus*, and *B. fermus* and wherein said truncated pullulanase is capable of catalyzing the hydrolysis of an alpha-1,6-glucosidic bond.

7. (Twice amended) A truncated *Bacillus* pullulanase comprising a deletion of about 200 amino acids from the amino terminus of a *Bacillus* pullulanase wherein the *Bacillus* is selected from the group consisting of *B. subtilis*, *B. deramificans*, *B. stearothermophilus*, *B. naganoensis*, *B. flavocaldarius*, *B. acidopullulyticus*, *Bacillus* sp APC-9603, *B. sectorramus*, *B. cereus*, and *B. fermus* and wherein said truncated pullulanase is capable of catalyzing the hydrolysis of an alpha-1,6-glucosidic bond.

8. (Twice amended) A truncated *Bacillus* pullulanase comprising a deletion of about 300 amino acids from the amino terminus of a *Bacillus* pullulanase wherein the *Bacillus* is selected from the group consisting of *B. subtilis*, *B. deramificans*, *B. stearothermophilus*, *B. naganoensis*, *B. flavocaldarius*, *B. acidopullulyticus*, *Bacillus* sp APC-9603, *B. sectorramus*, *B. cereus*, and *B. fermus* and wherein said truncated pullulanase is capable of catalyzing the hydrolysis of an alpha-1,6-glucosidic bond.

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9. (Twice amended) A truncated *Bacillus* pullulanase comprising a deletion that is 98 amino acids from the amino terminus of *Bacillus deramificans* pullulanase, wherein said truncated pullulanase is capable of catalyzing the hydrolysis of an alpha-1,6-glucosidic bond.

10. (Twice amended) A truncated *Bacillus* pullulanase comprising a deletion that is 102 amino acids from the amino terminus of *Bacillus deramificans* pullulanase, wherein said truncated pullulanase is capable of catalyzing the hydrolysis of an alpha-1,6-glucosidic bond.

11. (Twice amended) A modified *Bacillus* pullulanase which is capable of catalyzing the hydrolysis of an alpha-1,6-glucosidic bond, wherein the modification is an addition of at least one amino acid to the amino terminus of the mature pullulanase amino acid sequence obtainable from *Bacillus deramificans*.

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S-2
12. (Twice amended) The pullulanase of Claim 11, wherein the additional amino acid at the amino terminus is an Alanine.

S-2
14. (Twice Amended) A truncated *Bacillus* pullulanase produced by a method comprising the steps of

S-2
a) obtaining a recombinant host cell comprising nucleic acid encoding mature pullulanase having at least 70% identity to the polynucleotide sequence as shown in SEQ ID NO:1,

S-2
b) culturing said host cell under conditions suitable for the production of a truncated pullulanase, and

D-2
c) recovering the truncated pullulanase wherein the truncated *Bacillus* pullulanase comprises a deletion of about 100 amino acids from the amino terminus of a *Bacillus* pullulanase

S-2
wherein the *Bacillus* is selected from the group consisting of *B. subtilis*, *B. deramificans*, *B. stearothermophilus*, *B. naganoensis*, *B. flavocaldarius*, *B. acidopullulyticus*, *Bacillus* sp APC-9603, *B. sectorramus*, *B. cereus*, and *B. fermus* and said truncated pullulanase is capable of catalyzing the hydrolysis of an alpha-1,6-glucosidic bond.

S-2
15. (Twice amended) The pullulanase of Claim 14, wherein said host cell is *B. licheniformis* which comprises a first gene encoding Carlsberg protease and a second gene encoding endo Glu C protease, the first and/or second gene which codes for the protease(s) having been altered such that the protease(s) is/are inactivated.

D-3
27. (Twice amended) An enzymatic composition comprising a truncated *Bacillus* pullulanase wherein said truncated pullulanase is selected from the group of pullulanases consisting of

S-2
a) a deletion of up to about 100 amino acids from the amino terminus of a *Bacillus* pullulanase,

S-2
b) a deletion of up to about 200 amino acids from the amino terminus of a *Bacillus* pullulanase, and

S-2
c) a deletion of up to about 300 amino acids from the amino terminus of a *Bacillus* pullulanase,

S-2
wherein the *Bacillus* is selected from the group consisting of *B. subtilis*, *B. deramificans*, *B. stearothermophilus*, *B. naganoensis*, *B. flavocaldarius*, *B. acidopullulyticus*, *Bacillus* sp APC-9603, *B. sectorramus*, *B. cereus*, and *B. fermus* and

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Sub
Sub

wherein said truncated pullulanase is capable of catalyzing the hydrolysis of an alpha-1,6-glucosidic bond.

D3

28. (Twice amended) The enzymatic composition of Claim 27, wherein the pullulanase has a deletion of up to about 100 amino acids from the amino terminus.

D3

29. (Twice amended) The enzymatic composition of Claim 27, wherein the pullulanase has a deletion of up to about 200 amino acids from the amino terminus.

Sub
Sub

30. (Twice amended) The enzymatic composition of Claim 27, wherein the pullulanase has a deletion of up to about 300 amino acids from the amino terminus.

Sub
Sub

31. (Twice Amended) An enzymatic composition comprising the pullulanase of Claim 9, wherein the pullulanase has the amino acid sequence as shown in SEQ ID NO: 2 beginning at amino acid residue 99, a glutamic acid.

Add
E5

32. (Twice Amended) An enzymatic composition comprising the pullulanase of Claim 10, wherein the pullulanase has the amino acid sequence as shown in SEQ ID NO: 2 beginning at amino acid residue 103, a glutamic acid.